

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on January 16, 2003, 16:39:12, Search time 20.4 seconds
(without alignments)
28.454 Million cell updates/sec

Title: US-09-856-070-17

Perfect score: 69

Sequence: 1 ERKEQMMREKEEL 14

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 6

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Swissprot_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	69	100.0	580	1	EZRI_HOVIN
2	69	100.0	585	1	EZRI_HOVIN
3	66	95.7	585	1	MOES_MOUSE
4	51	73.9	576	1	MOES_HUMAN
5	51	73.9	576	1	MOES_MOUSE
6	51	73.9	576	1	MOES_PIG
7	51	73.9	583	1	RADI_HUMAN
8	51	73.9	583	1	RADI_MOUSE
9	51	73.9	583	1	RADI_PIG
10	47	68.1	1549	1	TPHY_SHEEP
11	46	66.7	2564	1	SPOL_HUMAN
12	43	62.3	121	1	ABRA_FLATF
13	43	62.3	743	1	ABRA_FLATF
14	43	62.3	1157	1	V182_HUMAN
15	43	62.3	1344	1	IF3A_MOUSE
16	43	62.3	1382	1	IF3A_HUMAN
17	43	62.3	1407	1	TRHY_PABIT
18	43	62.3	1808	1	TRHY_HUMAN
19	42	60.9	123	1	RIFA_NEIMA
20	42	60.9	123	1	RIFA_NEIMA
21	42	60.9	216	1	PRP6_YEAST
22	42	60.9	471	1	VAL5_SCHUG
23	42	60.9	514	1	ZBFL_MOUSE
24	42	60.9	4587	1	ELEL_PAT
25	41	59.4	85	1	IATP_YEAST
26	41	59.4	243	1	TRIC_XENIA
27	41	59.4	386	1	NISC_HUMAN
28	41	59.4	419	1	NEMO_HUMAN
29	41	59.4	476	1	MPPB_NEUCR
30	41	59.4	877	1	INPE_HICOF
31	41	59.4	2068	1	TZDI_DROME
32	40	58.0	180	1	PTTG_HUMAN
33	40	58.0	249	1	PSEL_MOUSE

34	40	58.0	462	1	MPPB_YEAST
35	40	58.0	466	1	CYP8_CAMEL
36	40	58.0	503	1	CP39_RAT
37	40	58.0	503	1	CP30_MOUSE
38	40	58.0	592	1	GP1_HUMAN
39	40	58.0	1959	1	MYH9_CHICK
40	40	58.0	1960	1	MYH9_HUMAN
41	40	58.0	4473	1	PIEL_CRICR
42	39	56.5	148	1	SSRP_RALSO
43	39	56.5	309	1	MATL_XENLA
44	39	56.5	330	1	RLX3_STRAU
45	39	56.5	341	1	TZD6_MOUSE

ALIGNMENTS

RESULT 1					
EZRI_HOVIN					
ID	EZRI_HOVIN	STANDARD:	PR1:	580 AA.	
AC	F31976				
DT	01-JUL-1993 (Rel. 26, Created)				
DT	01-JUL-1993 (Rel. 26, Last sequence update)				
DT	16-OCT-2001 (Rel. 40, Last annotation update)				
DE	Ezrin (p81) (Cytoovillin) (Villin 2).				
GN	VIL2.				
OS	Bos taurus (Bovine).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;				
OC	Bovidae; Bovinae; Bos.				
OX	NCHI_TaxID=9913;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
FC	ISSUE-Brain;				
RA	Bergson C.M., Zhao H., Salih K., Duman R.S., Nestler E.J.;				
RT	"Ezrin and osteonectin, two proteins associated with cell shape and growth, are enriched in the locus coeruleus."				
RL	Mol. Cell. Neurosci. 4:64-73(1993).				
RN	[2]				
RP	SEQUENCE OF 1-15 AND 126-140.				
TI	TISSUE-Kidney;				
KX	MEDLINE 96239137; PubMed-8660651;				
RA	Galat A., Gerbed M.C., Boest F., Riviere S.;				
RT	"Ezrins and their arming and compositions uniqueness, variability, and applications."				
RL	Arch. Biochem. Biophys. 330:229-237(1996).				
CC	FUNCTION: PROBABLY INVOLVED IN CONNECTIONS OF MAJOR CYTOSKELETAL STRUCTURES TO THE PLASMA MEMBRANE.				
CC	SUBCELLULAR LOCATION: MICROVILLAR PERIPHERAL MEMBRANE PROTEIN (CYTOPLASMIC SIDE).				
CC	PTM: PHOSPHORYLATED BY PROTEIN-TYROSINE KINASES.				
CC	SIMILARITY: CONTAINS 1 BAND 4.1-LIKE DOMAIN.				
CC	THIS SWISS PROTEIN ENTRY IS COPYRIGHTED. IT IS PRODUCED THROUGH A COLLABORATION between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non profit institutions as long as its content is in the way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. Usage by and for commercial or send an email to license@isb.sib.ch .				
CC	EMBL: M98498; AAA40510.1;				
DP	InterPro: IPR000299; Band_4.1.				
DR	InterPro: IPR000798; Ezrin/moesin.				
DR	Pfam: PF00373; Band_4.1; 1.				
DR	Pfam: PF00769; ERM; 1.				
DR	PRINTS: PR00935; HAND41.				
DR	SMART: SM00295; H41; 1.				
DR	PROSITE: PS00660; BAND_4.1; 1.				
DR	PROSITE: PS00661; BAND_4.1; 1.				
DR	PROSITE: PS00657; BAND_4.1; 1.				
KW	Structural protein, Cytoskeleton, Phosphorylation.				
FT	INIL_MET 0				

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FI DOMAIN 57 224 BAND 4.1-LIKE.
FI MOD_RES 145 145 PHOSPHORYLATION (BY PDGFR)
FI MOD_RES 353 353 (BY SIMILARITY)
FI MOD_RES 353 353 PHOSPHORYLATION (BY PDGFR)
FI MOD_RES 353 353 (BY SIMILARITY)
SQ SEQUENCE 580 AA; 68629 MW; 8CD6635C200FAA3 CRC64;

Query Match 100.0%; Score 69; DB 1; Length 580;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EREKQMMREKEEL 14
DD 333 EREKQMMREKEEL 346
|||||

RESULT 4
EZRI_HUMAN
AC P15111; P23714; Q9NSJ4; PRI; 585 AA.
DT 01-APR-1996 (Rel. 14, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ezrin (p81) (Cytovillin) (Villin 2);
GN Vill2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SQ SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
RX MEDLINE-90076135; PubMed-2591371;
RA Gould K.L., Bretscher A., Esch F.S., Hunter T.;
RT "cDNA cloning and sequencing of the protein-tyrosine kinase
RT substrate, ezrin, reveals homology to band 4.1.";
RL EMBO J. 8:4133-4142(1989).
RN [2]
SQ SEQUENCE FROM N.A.
RX MEDLINE-92406868; PubMed-1382070;
RA Turunen O., Winkvist P., Pakkanen R., Grzeschik K.-H., Wahlstromer T.,
RA Valeri A.;
RT "Cytovillin, a microvillar Mr 75,000 protein, cDNA sequence,
RT prokaryotic expression, and chromosomal localization.";
RL J. Biol. Chem. 264:16727-16732(1989).
RN [3]
SQ SEQUENCE FROM N.A.
RA Ottenwaelder B., Germaier B., Mewes H. W., Weil R., Wiemann S.;
RL Submitted (MAP-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
SQ SEQUENCE OF 171-179 AND 342-349.
RX MEDLINE-96311348; PubMed-8713105;
RA Egeron M., Moritz P. I., Decker E., Kelso A., Simpson P. I.;
RT "Identification of the 70kd heat shock cognate protein (Hsc70) and
RT alpha-actinin-1 as novel phosphotyrosine containing proteins in T
RT lymphocytes.";
RL Biochem. Biophys. Res. Commun. 224:666-674(1996).
RN [5]
SQ PHOSPHORYLATION BY PDGFR.
RX MEDLINE-92406868; PubMed-1382070;
RA Krieg J., Hunter T.;
RT "Identification of the two major epidermal growth factor induced
RT tyrosine phosphorylation sites in the microvillar core protein
RT ezrin.";
RL J. Biol. Chem. 267:19258-19265(1992).
RN [6]
SQ PHOSPHORYLATION.
RX MEDLINE-92388649; PubMed-1381389;
RA Egeron M., Burgess W. H., Chen D., Decker B. J., Bretscher A.,
RA Samuelson L.E.;
RT "Identification of ezrin as an 81-kDa tyrosine-phosphorylated protein
RT in T cells.";
RL J. Immunol. 149:1847-1852(1992).

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-1- FUNCTION: PROBABLY INVOLVED IN CONNECTIONS OF MAJOR CYTOSKELETAL
CC STRUCTURES TO THE PLASMA MEMBRANE.
CC -1- SUBCELLULAR LOCATION: MICROVILLAR PERIPHERAL MEMBRANE PROTEIN
CC (CYTOPLASMIC SIDE).
CC -1- TISSUE SPECIFICITY: COMPONENT OF THE MICROVILLI OF INTESTINAL
CC EPITHELIAL CELLS.
CC -1- PTM: PHOSPHORYLATED BY PROTEIN-TYROSINE KINASES.
CC -1- SIMILARITY: CONTAINS 1 HAND 4.1-LIKE DOMAIN.
CC
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CC
CC EMBL: X51521; CAA35893.1; -.
CC EMBL: J05021; AAA61278.1; ALT_INIT.
CC EMBL: A1162086; CAH82418.1; ALT_INIT.
CC PIR: S09263; S09263.
CC PIR: A34400; A34400.
CC SWISS-2DPAGE: P15311; HUMAN.
CC GENE: HENC12691; Vill2.
CC MIM: 123900; -.
CC InterPro: IPR000299; Hand_4.1.
CC InterPro: IPR000798; Ez/rad/moesin.
CC Pfam: PF00373; Band_41; 1.
CC Pfam: PF00769; ERM_1.
CC PRINTS: PR00935; HAND41.
CC SMART: SM00295; H41; 1.
CC PROSITE: PS00660; HAND_41_1; 1.
CC PROSITE: PS00661; BAND_41_2; 1.
CC PROSITE: PS00507; BAND_41_3; 1.
CC Structural protein; Cytoskeleton; Phosphorylation.
KW INIT_MET 0
FT DOMAIN 57 224 HAND 4.1-LIKE.
FT MOD_RES 145 145 PHOSPHORYLATION (BY PDGFR).
FT MOD_RES 353 353 PHOSPHORYLATION (BY PDGFR).
FT CONFLICT 531 531 V -> L (IN REF. 3).
SQ SEQUENCE 585 AA; 69267 MW; 2A844D140E3B0ACC CRC64;

Query Match 100.0%; Score 69; DB 1; Length 585;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EREKQMMREKEEL 14
DD 333 EREKQMMREKEEL 346
|||||

RESULT 3
EZRI_MOUSE
AC P26040; STANDARD; PRI; 585 AA.
DE 01-MAY-1992 (Rel. 22, Created)
DE 01-MAY-1992 (Rel. 22, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ezrin (p81) (Cytovillin) (Villin 2).
GN Vill2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SQ SEQUENCE FROM N.A.
RX MEDLINE-92064635; PubMed-1955455;
RA Funayama N., Nagafuchi A., Sato N., Tsukita S., Tsukita S.;
RT "Radixin is a novel member of the band 4.1 family.";
RL J. Cell Biol. 115:1039-1048(1991).
CC -1- FUNCTION: PROBABLY INVOLVED IN CONNECTIONS OF MAJOR CYTOSKELETAL
CC STRUCTURES TO THE PLASMA MEMBRANE.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.

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EMBL: S47577; AAA11762.1; -;
EMBL: M86390; AAA39728.1; -;
MGD: MGI:97167; Msn.
InterPro: IPR000299; Band_4.1.
InterPro: IPR000798; Ez/rad/moesin.
Pfam: PF00373; Band_41; 1.
Pfam: PF00769; Band_41; 1.
PRINTS: PR00935; BAND41.
SMART: SM00295; B41; 1.
PROSITE: PS00660; BAND_41_1; 1.
PROSITE: PS00661; BAND_41_2; 1.
PROSITE: PS00557; BAND_41_3; 1.
KW Structural protein; Cytoskeleton.
FT INIT-MET 0 BY SIMILARITY.
FT DOMAIN 57 224 BAND 4.1-LIKE.
FT CONFLICT 430 331 EL -> DV (IN REF. 2).
FT CONFLICT 370 371 RA -> SP (IN REF. 2).
SQ SEQUENCE 576 AA: 67635 MW: 50F455552E9145 CRC64;

Query Match 73.9% Score 51; DB 1; Length 576;
Best Local Similarity 71.4%; Pred. No. 3.9;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EREKEOMREKEEL 14
I:||||| I:|||||
Db 333 EKEKEIEREKEEL 346

RESULT 6

MOES_PIG STANDARD; PRT; 576 AA.
AC P26042;
DI 01-MAY-1992 (Rel. 22, Created)
DI 01-AUG-1992 (Rel. 23, Last sequence update)
DI 16-OCT-2001 (Rel. 40, Last annotation update)
DE Moesin (Membrane organizing extension spike protein).
GN MSN.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
FN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-94092743; PubMed 8268231;
RA Larkes W.T., Schwartz Albiec K., Furlimayr H.,
RT Cloning and sequencing of porcine moesin and radixin cDNA and
RT identification of highly conserved domains.*;
RL Biochim. Biophys. Acta 1216:479-482(1993).
CC -1- FUNCTION: PROBABLY INVOLVED IN CONNECTIONS OF MAJOR CYTOSKELETAL
CC STRUCTURES TO THE PLASMA MEMBRANE
CC -1- SIMILARITY: CONTAINS 1 HAND 4.1-LIKE DOMAIN.
CC
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EMBL: M86450; AAB02864.1; -;
PIR: S39804.
InterPro: IPR000299; Band_4.1.
InterPro: IPR000798; Ez/rad/moesin.
Pfam: PF00373; Band_41; 1.
Pfam: PF00769; ERM; 1.
PRINTS: PR00935; BAND41.
KW Structural protein; Cytoskeleton; Actin-binding; Capping protein.
FT DOMAIN 58 225 BAND 4.1-LIKE.
FT CONFLICT 470 477 POLY-PRO.
SQ SEQUENCE 583 AA: 66564 MW: 889687E1D675FFE7 CRC64;

DR SMART: SM00295; B41; 1.
DR PROSITE: PS00660; BAND_41_1; 1.
DR PROSITE: PS00661; BAND_41_2; 1.
DR PROSITE: PS00557; BAND_41_3; 1.
KW Structural protein; Cytoskeleton.
FT INIT-MET 0 BY SIMILARITY.
FT DOMAIN 57 224 BAND 4.1-LIKE.
FT CONFLICT 430 331 EL -> DV (IN REF. 2).
FT CONFLICT 370 371 RA -> SP (IN REF. 2).
SQ SEQUENCE 576 AA: 67529 MW: 3CE0BF78E3F75E6B CRC64;

Query Match 73.9% Score 51; DB 1; Length 576;
Best Local Similarity 71.4%; Pred. No. 3.9;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EREKEOMREKEEL 14
I:||||| I:|||||
Db 333 EKEKEIEREKEEL 346

RESULT 7

RADI_HUMAN STANDARD; PRT; 583 AA.
ID P35241;
DI 01-FEB-1994 (Rel. 28, Created)
DI 01-FEB-1994 (Rel. 28, Last sequence update)
DI 16-OCT-2001 (Rel. 40, Last annotation update)
DE Radixin.
GN RDX.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
FN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-93252378; PubMed-8486357;
RA Wilgenbus K.K., Milatovich A., Francke U., Furlimayr H.,
RT Molecular cloning, cDNA sequence, and chromosomal assignment of the
RT human radixin gene and two dispersed pseudogenes.*;
RL Genomics 16:199-206(1993).
CC -1- FUNCTION: PROBABLY PLAYS A CRUCIAL ROLE IN THE BINDING OF THE
CC BARBED END OF ACTIN FILAMENTS TO THE PLASMA MEMBRANE
CC -1- SUBCELLULAR LOCATION: HIGHLY CONCENTRATED IN THE UNDERCUT OF THE
CC CELL-TO-CELL ADHERENS JUNCTION AND THE CLEAVAGE FURROW IN THE
CC INTERPHASE AND MITOTIC PHASE, RESPECTIVELY.
CC -1- SIMILARITY: CONTAINS 1 HAND 4.1-LIKE DOMAIN.
CC
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EMBL: L02320; AAA36541.1; -;
PIR: A46127; A46127; 2501; IEF.
Aarhus/Chent-2DPAGE; RDX.
Genew: H0NC:9944; RDX.
MIM: 179410;
InterPro: IPR000299; Band_4.1.
InterPro: IPR000798; Ez/rad/moesin.
Pfam: PF00373; Band_41; 1.
Pfam: PF00769; ERM; 1.
PRINTS: PR00935; BAND41.
SMART: SM00295; B41; 1.
PROSITE: PS00660; BAND_41_1; 1.
PROSITE: PS00661; BAND_41_2; 1.
PROSITE: PS00557; BAND_41_3; 1.
KW Structural protein; Cytoskeleton; Actin-binding; Capping protein.
FT DOMAIN 58 225 BAND 4.1-LIKE.
FT CONFLICT 470 477 POLY-PRO.
SQ SEQUENCE 583 AA: 66564 MW: 889687E1D675FFE7 CRC64;

Query Match 73.9% Score 51; DB 1; Length 583;
 Best Local Similarity 71.4% Pred. No. 4;
 Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EREKQMMREKEEL 14

DB 334 EREKRIEREREKEEL 347

RESULT 8

ID RADL_MOUSE

AC P26043; STANDARD; PRT; 583 AA.

DI 01-MAY-1992 (Rel. 22, Created)

DT 01-MAY-1992 (Rel. 22, Last sequence update)

DE 16-OCT-2001 (Rel. 40, Last annotation update)

DE Radixin

GN RDX

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

OX NCBI_TaxID-10090;

RN [1]

PP SEQUENCE FROM N.A. AND SEQUENCE OF 28-53 AND 263-277.

KC TISSUE=Liver;

PX MEDLINE-92054635; PubMed-1955155;

RA Funayama N., Nagaiuchi A., Sato N., Tsukita S., Tsukita S.;

FT "Radixin is a novel member of the Band 4.1 family. "

RL J. Cell Biol. 115:1039-1048(1991).

CC -1- FUNCTION: PROBABLY PLAYS A CRUCIAL ROLE IN THE BINDING OF THE

CC BARBED END OF ACTIN FILAMENTS TO THE PLASMA MEMBRANE.

CC -1- SUBCELLULAR LOCATION: HIGHLY CONCENTRATED IN THE UNDERCOAT OF THE

CC CELL-TO-CELL ADHERENS JUNCTION AND THE CLEAVAGE FURROW IN THE

CC INTERPHASE AND MITOTIC PHASE, RESPECTIVELY.

CC -1- SIMILARITY: CONTAINS 1 BAND 4.1-LIKE DOMAIN.

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CC EMBL; X60672; cMA4.0047 1;

DR PIR; A41129; A41129.

DR MGD; MGI-97887; Pdx.

DR InterPro; IPR000299; Band_4.1.

DR InterPro; IPR000798; P2/rad/moesin.

DR Pfam; PF00373; Band_41; 1.

DR Pfam; PF00769; EPM; 1.

DR PRINTS; PR00935; BAND41.

DR SMART; SM00295; B41; 1.

DR PROSITE; PS00660; BAND_41_1; 1.

DR PROSITE; PS00661; BAND_41_2; 1.

DR PROSITE; PS00662; BAND_41_3; 1.

KW Structural protein; Cytoskeleton; Actin-binding; Capping protein.

FT DOMAIN 58 225 BAND 4.1-LIKE.

FT DOMAIN 470 477 POLY-PRO.

SQ SEQUENCE 583 AA; 68451 MW; 3219A52ECDC871BE CRC64;

Query Match 73.9% Score 51; DB 1; Length 583;

Best Local Similarity 71.4% Pred. No. 4;

Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EREKQMMREKEEL 14

DB 334 EREKRIEREREKEEL 347

RESULT 9

ID RADL_PIG

AC P26043; STANDARD; PRT; 583 AA.

P26044;

DI 01-MAY-1992 (Rel. 22, Created)

DT 01-MAY-1992 (Rel. 22, Last sequence update)

DE 16-OCT-2001 (Rel. 40, Last annotation update)

DE Radixin (Moesin B).

GN RDX.

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI_TaxID-9823;

RN [1]

PP SEQUENCE FROM N.A.

PX MEDLINE-94052713; PubMed-8268231;

RA Laikes W.L., Schwartz Albiez R., Fortlindyr H.;

FT "Cloning and sequencing of porcine moesin and radixin cDNA and

FT identification of highly conserved domains. "

PL Biochim Biophys Acta 1216:479-482(1993).

CC -1- FUNCTION: PROBABLY PLAYS A CRUCIAL ROLE IN THE BINDING OF THE

CC BARBED END OF ACTIN FILAMENTS TO THE PLASMA MEMBRANE.

CC -1- SUBCELLULAR LOCATION: HIGHLY CONCENTRATED IN THE UNDERCOAT OF THE

CC CELL-TO-CELL ADHERENS JUNCTION AND THE CLEAVAGE FURROW IN THE

CC INTERPHASE AND MITOTIC PHASE, RESPECTIVELY.

CC -1- SIMILARITY: CONTAINS 1 BAND 4.1-LIKE DOMAIN.

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EMBL; M8444; AAB02865.1; -

DR PIR; S39805; S39805.

DR InterPro; IPR000299; Band_4.1.

DR InterPro; IPR000798; P2/rad/moesin.

DR Pfam; PF00373; Band_41; 1.

DR Pfam; PF00769; EPM; 1.

DR PRINTS; PR00935; BAND41.

DR SMART; SM00295; B41; 1.

DR PROSITE; PS00660; BAND_41_1; 1.

DR PROSITE; PS00661; BAND_41_2; 1.

DR PROSITE; PS00662; BAND_41_3; 1.

KW Structural protein; Cytoskeleton; Actin-binding; Capping protein.

FT DOMAIN 58 225 BAND 4.1-LIKE.

FT DOMAIN 470 477 POLY-PRO.

SQ SEQUENCE 583 AA; 68549 MW; 59AE286DCAF7397 CRC64;

Query Match 73.9% Score 51; DB 1; Length 583;

Best Local Similarity 71.4% Pred. No. 4;

Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EREKQMMREKEEL 14

DB 334 EREKRIEREREKEEL 347

RESULT 10

ID TRHY_SHEEP

AC P22793; STANDARD; PRT; 1549 AA.

DI 01-AUG-1991 (Rel. 19, Created)

DT 01-OCT-1994 (Rel. 30, Last sequence update)

DE 15-JUN-2002 (Rel. 41, Last annotation update)

DE Trichohyalin.

GN THH.

OS Ovis aries (Sheep).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Caprinae; Ovis.

OX NCBI_TaxID-9940;

RN [1]

PP SEQUENCE FROM N.A.

SEQUENCE FROM N.A. (ISOFORMS 1 TO 4).
 MEDLINE=20539976; PubMed=11046001;
 RA Berghs S, Arquero P, Dirks P, Jr, Maksimova E, Svabach P,
 RA Hermel J-M, Zhang J-P, Philbrick W, Slepnev V, Ort T.,
 RA Solimena M.
 RT "beta1 spectrin, a new spectrin localized at axon initial segments
 RT and nodes of Ranvier in the central and peripheral nervous system";
 RL J. Cell Biol 151:995-1002(2000)
 RN [3]
 PP SEQUENCE OF 386-2382 FROM N.A. (ISOFORM 1).
 RC TISSUE=Brain;
 RX MEDLINE=20450483; PubMed=10947877;
 RA Nagase T, Kikuno R, Nakayama M, Ohara G,
 RT "Prediction of the coding sequences of unidentified human genes.
 RT XVIII. The complete sequences of 100 new cDNA clones from brain which
 RT code for large proteins in vitro";
 PL DNA Res 7:273-281(2000)
 CC -!- ALTERNATIVE PRODUCTS: 4 isoforms; 1 (shown here), 2, 3 and 4, are
 CC produced by alternative splicing.
 CC -!- TISSUE SPECIFICITY: Abundantly expressed in brain and pancreatic
 CC islets.
 CC -!- SIMILARITY: BELONGS TO THE SPECTRIN FAMILY.
 CC -!- SIMILARITY: CONTAINS 2 CALPUNIN-BINDING (CH) DOMAINS
 CC -!- SIMILARITY: CONTAINS 1 PH DOMAIN.
 CC -!- SIMILARITY: CONTAINS 18 SPECTRIN REPEATS.
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REPEAT 1199 1303 SPECTRIN 10.
 REPEAT 1395 1498 SPECTRIN 11.
 REPEAT 1410 1513 SPECTRIN 12.
 REPEAT 1515 1619 SPECTRIN 13.
 REPEAT 1621 1725 SPECTRIN 14.
 REPEAT 1727 1832 SPECTRIN 15.
 REPEAT 1834 1940 SPECTRIN 16.
 REPEAT 1942 2046 SPECTRIN 17.
 REPEAT 2048 2107 SPECTRIN 18.
 PH
 MISSING (IN ISOFORM 3).
 AVAAALGRLKQCNITAGLAAVIRLLEK > MIPHYSCS
 SAFPSTPTTPGQGLEAPHR (IN ISOFORM 4).
 NENQNLKAVQWQKHLHQLELDR -> CLILHPALLHDPWE
 PNYLPSSS (IN ISOFORM 2).
 MISSING (IN ISOFORM 3).
 IETKRAELSKQETHTLGGFFETGTELAKAAKATLELERY
 E -> PRRLHLPNGVQWQWHLNPSLQPKRANKETAR
 RGTGL (IN ISOFORM 4).
 MISSING (IN ISOFORM 4).
 MISSING (IN REF. 2).
 L -> S (IN REF. 2).
 E -> K (IN REF. 2).
 E -> K (IN REF. 2).
 G -> S (IN REF. 1).
 SQ SEQUENCE 2564 AA; 248982 MW; 530870111061EPC QRC64;
 Query Match 66.7%. Score 46, DB 1. Length 2564;
 Best Local Similarity 64.3%; Pred. No. 84;
 Matches 3, Conservative 3, Mismatches 2, Indels 0; Caps 0;
 QY 1 EREKQMMREKEEL 14
 DB 1364 EREGQLMQEKPEL 1377
 RESULT 12
 ID ABRA_PLAFT STANLAKO, PRI, 321 AA.
 AC P23746;
 DT 01-NOV-1991 (Ref. 20, Created)
 DT 01-NOV 1991 (Ref. 20, Last sequence update)
 DT 01-FEB 1994 (Ref. 28, Last annotation update)
 DE 101 kDa malaria antigen (PI01) (Acidic basic repeat antigen)
 DE (Fragment).
 GN ABRA.
 OS Plasmodium falciparum (isolate FC27 / Papua New Guinea).
 CC Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
 CX NCBI_TaxID=5837;
 KX [1]
 KP SEQUENCE FROM N.A.
 RX MEDLINE=87038741; PubMed=3534513;
 RA Stahl H-D, Bianco A-E, Grewther P-E, Anders R-F, Kyne A-P,
 RA Coppel R-L, Mitchell G-F, Kemp D-J, Brown G-V;
 RT "Sorting large numbers of clones expressing plasmodium falciparum
 RT antigens in Escherichia coli by differential antibody screening";
 RL Mol. Biol. Med. 3:391-398(1986).
 CC -!- SUBCELLULAR LOCATION: AT THE MEMBRANE SURFACE AND WITHIN THE
 CC PARASITOPHOUS VACUOLE.
 CC -!- PIM: NOT GLYCOSYLATED (PROBABLE).
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 DR EMBL: M15514; AAA29463.1;
 KW Antigen; Malaria; Repeat.
 FT NON_TER 1
 FT DOMAIN 275 >321 TANDEM REPEATS OF K-E(2,3).

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FI NON_TER 421 321
SO SEQUENCE 321 AA 37805 MW: 08844A0681E0714R CPO64;

Query Match 62.3%; Score 43; DB 1; Length 321;
Best Local Similarity 61.5%; Pred. No. 27;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 EREKQMMKEKEE 13
I:|||||
DB 290 EKEKEKEKEKEE 302

RESULT 13
ABRA_PLAFC
ID ABRA_PLAFC STANVAP; PRT: 743 AA.
AC P25620;
UT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DE 15-JUL-1998 (Rel. 36, Last annotation update)
DE 101 kDa malaria antigen (PI01) (Acidic basic repeat antigen).
GN ABRA.
OS Plasmodium falciparum (isolate Camp / Malaysia)
OC Eukaryota; Alveolata; Apicomplexa; Euarchaezoa; Plasmodium.
OX NCBI_TaxID=5835;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88298794; PubMed=3042768;
RA Weber J.L., Lyon T.A., Wolff P.H., Hall T., Lowell G.H., Chelley J.D.;
RT "Primary structure of a Plasmodium falciparum malaria antigen located at the merozoite surface and within the parasitophorous vacuole."
RL J. Biol. Chem. 263:11421-11425 (1988).
CC -!- SURCELLULAR LOCATION: AT THE MEROZOITE SURFACE AND WITHIN THE PARASITOPHOUS VACUOLE.
CC -!- PTM: NOT GLYCOSYLATED (PROBABLE).
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CC -----
DR EMBL: J04902; AAA29462.1;
SR PIR: A29232; A29232.
KW Antigen; Malaria; Repeat.
FT DOMAIN 226 273 8 X 6 AA REPEATS OF [VT]-N-D [ED] [ED]-D.
FT REPEAT 226 273
FT REPEAT 226 231
FT REPEAT 232 237
FT REPEAT 238 243
FT REPEAT 244 249
FT REPEAT 250 255
FT REPEAT 256 261
FT REPEAT 262 267
FT REPEAT 268 273
FT DOMAIN 674 731 LNDPM REPEATS OF K-E(2.3).
SQ SEQUENCE 743 AA: 86622 MW: FBF0BF8B07D922C CRC64;

Query Match 62.3%; Score 43; DB 1; Length 743;
Best Local Similarity 61.5%; Pred. No. 62;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 EREKQMMKEKEE 13
I:|||||
DB 694 EKEKEKEKEKEE 706

RESULT 14
Y182_HUMAN
ID Y182_HUMAN STANDARD; PRT: 1157 AA.
AC Q14687;
DT 01-NOV-1997 (Rel. 35, Last sequence update)

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DI 16-OCT-2001 (Rel. 40, Last annotation update)
DI Hypothetical protein KIAA0182 (Fragment).
GN KIAA0182.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
EX MEDLINE 96281124; PubMed 8724849;
RA Nagase T., Seki N., Ishikawa K.-I., Tanaka A., Nomura N.;
RT "Prediction of the coding sequences of unidentified human genes. V. The coding sequences of 40 new genes (KIAA0161-KIAA200) deduced by analysis of cDNA clones from human cell line KG-1."
RL DNA Res. 3:17-24 (1996).
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CC -----
DR EMBL: D80004; HA11499.1;
KW Hypothetical protein.
FT NCN_TER 1
FT DOMAIN 591 596 POLY-PRO.
FT DOMAIN 685 688 POLY-ARG.
FT DOMAIN 1042 1047 POLY-GLU.
SQ SEQUENCE 1157 AA: 130323 MW: H01A0AF5A6FAH5FH CRC64;

Query Match 62.3%; Score 43; DB 1; Length 1157;
Best Local Similarity 64.3%; Pred. No. 97;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EREKQMMKEKEE 14
I:|||||
DB 326 EREKQMMKEKEE 339

RESULT 15
IF3A_MOUSE
ID IF3A_MOUSE STANDARD; PRT: 1344 AA.
AC P23116; Q60697; Q62162;
DT 01-NOV-1991 (Rel. 20, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Eukaryotic translation initiation factor 3 subunit 10 (eIF-3 theta)
DE (eIF3 p167) (eIF3 p180) (eIF3 p185) (p162 protein) (Centrosomin).
GN EIF3S10 OR EIF3 OR CSNA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphoma;
RA Fisher R., Fillmore H., Reynolds A.H.;
RT "Molecular cloning and characterization of the 16.2 kDa component of a multi-protein complex phosphorylated by Src."
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 514-961 FROM N.A. (CENTROSOMIN B).
RX MEDLINE=98039715; PubMed=9372446;
RA Petzelt C., Joswig G., Mineheva A., Richter P., Stammer H., Werner D.;
RT "The centrosomal protein centrosomin A and the nuclear protein centrosomin B derive from one gene by post-transcriptional processes involving RNA editing."
RL J. Cell Sci. 110:2573-2578 (1997).
RN [3]
RP SEQUENCE OF 514-790 FROM N.A. (CENTROSOMIN A).

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